#2

ERROR DETECTED **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/714449

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
Numbering   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences
(OLD RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
(NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
(NEW RULES)   Sequence(s) _____ are missing this mandatory field or its response.

119-119 (and more)

12 _____ Use of <220>Feature
(NEW RULES)   Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING   DATE: 12/01/2000
PATENT APPLICATION: US/09/714,449   TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

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 3 <110> APPLICANT: Vogeli, Gabriel
 4         Huff, Rita
 5         Sejlitz, Torsten
 6         Lind, Peter
 7         Slightom, Jerry
 8         Schellin, Kathleen
 9         Bannigan, Chris
10         Ruff, Valerie
11         Kaytes, Paul
12         Wood, Linda
13         Parodi, Luis
14         Hiebsch, Ronald
16 <120> TITLE OF INVENTION: Novel G Protein Coupled Receptors
18 <130> FILE REFERENCE: 00431PHRM293
20 <140> CURRENT APPLICATION NUMBER: US/09/714,449
20 <141> CURRENT FILING DATE: 2000-11-16
20 <150> PRIOR APPLICATION NUMBER: 60/165,838
21 <151> PRIOR FILING DATE: 1999-11-16
23 <150> PRIOR APPLICATION NUMBER: 60/198,568
24 <151> PRIOR FILING DATE: 2000-04-20
26 <150> PRIOR APPLICATION NUMBER: 60/166,071
27 <151> PRIOR FILING DATE: 1999-11-17
29 <150> PRIOR APPLICATION NUMBER: 60/166,678
30 <151> PRIOR FILING DATE: 1999-11-19
32 <150> PRIOR APPLICATION NUMBER: 60/173,396
33 <151> PRIOR FILING DATE: 1999-12-28
35 <150> PRIOR APPLICATION NUMBER: 60/184,129
36 <151> PRIOR FILING DATE: 2000-02-22
38 <150> PRIOR APPLICATION NUMBER: 60/185,421
39 <151> PRIOR FILING DATE: 2000-02-28
41 <150> PRIOR APPLICATION NUMBER: 60/185,554
42 <151> PRIOR FILING DATE: 2000-02-28
44 <150> PRIOR APPLICATION NUMBER: 60/186,530
45 <151> PRIOR FILING DATE: 2000-03-02
47 <150> PRIOR APPLICATION NUMBER: 60/186,811
48 <151> PRIOR FILING DATE: 2000-03-03
50 <150> PRIOR APPLICATION NUMBER: 60/188,114
51 <151> PRIOR FILING DATE: 2000-03-09
53 <150> PRIOR APPLICATION NUMBER: 60/190,310
54 <151> PRIOR FILING DATE: 2000-03-17
56 <150> PRIOR APPLICATION NUMBER: 60/190,800
57 <151> PRIOR FILING DATE: 2000-03-21
59 <150> PRIOR APPLICATION NUMBER: 60/201,190
60 <151> PRIOR FILING DATE: 2000-05-02
62 <150> PRIOR APPLICATION NUMBER: 60/203,111
63 <151> PRIOR FILING DATE: 2000-05-08
65 <150> PRIOR APPLICATION NUMBER: 60/207,094
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RAW SEQUENCE LISTING              DATE: 12/01/2000
PATENT APPLICATION:  US/09/714,449    TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

66 <151> PRIOR FILING DATE: 2000-05-25
68 <160> NUMBER OF SEQ ID NOS: 190
70 <170> SOFTWARE: PatentIn version 3.0
72 <210> SEQ ID NO: 1
73 <211> LENGTH: 1182
74 <212> TYPE: DNA
75 <213> ORGANISM: H.Sapiens
77 <400> SEQUENCE: 1
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80  cctagctcct gctgatctag ttggggctcc agagtgggga ggagaaaggc actttgaaac    120
82  ttctctgccc ttaccgtctt agccatcaaa ctctgagctg gagatagtga cgatgtgaca    180
84  ggaactttcc ctgggcctct ctgggccaca attcctggcc gagagaaaga ggaggaatga    240
86  ggtgagcacc ttcttcactc ctagggccat gtggtagagc tgcagtcgca cctccttctg    300
88  ccaataggca tagatgagtg ggttgagcag ggagttgccc acgccgagca gccacaggta    360
90  ccgttccagc actaggtaga ggtgacactc ctggcaggcc acctgcacaa tgccagtgat    420
92  aaggaagggg gtccaggata gagcaaagct cccaatgaga acagacacag tacgagagc     480
94  tttgaagtcg ctgggagtcc gtggggatcg ataacctcca gccatggctc ctgcatgttc    540
96  catctttcga atctgctggc tgtgcatgaa ggcaatcttg agcatgtcgc agtagaagaa    600
98  gacaaagagg agcatggctg ggaagaagcc aacgcaggag agggtcagca cgaagtgagg    660
100 gtgaaataca gcaaagaagc tgcactgccc tttgtaggca gtctgctgga acatggggat    720
102 tccgagtggg aggaagccaa tgaggtaaga cactaaccac agcccggcaa tgcaggcccc    780
104 ggccacgaac ccactcatga tcttcaagta gcggaagggc tgcttgatgg caaggtacct    840
106 gtcaaaggtg atcagcatga ccgtgaggac agaggcagct gcggaggaag tgacaaatgc    900
108 catccgcagg ctgcacaggg tcttctgtgt gggccgagaa ggctggaga gctggtctgt     960
110 gagtaggcca gagatggcca caccaatcaa ggtgtcagcc acagccagat tcaaggtgaa   1020
112 gcagagactg acaccatcat tcttgtggat caacagcagc acagccacag ccactagtgt   1080
114 gttagtagca atgatgaggg aggccaggac agcaaggatc actccaaatg agaaagatga   1140
116 ttccatgtct cgaagtggca ggacttcact taccagggca tg                      1182
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 335
121 <212> TYPE: PRT
122 <213> ORGANISM: H.Sapiens
124 <400> SEQUENCE: 2
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127 1               5                   10                  15
129 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
130             20                  25                  30
132 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
133         35                  40                  45
135 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
136     50                  55                  60
138 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
139 65                  70                  75                  80
141 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
142                 85                  90                  95
144 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
145             100                 105                 110
147 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
148         115                 120                 125
```

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RAW SEQUENCE LISTING              DATE: 12/01/2000
PATENT APPLICATION:  US/09/714,449   TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

150 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
151     130             135             140
153 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
154 145             150             155             160
156 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
157             165             170             175
159 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
160         180             185             190
162 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
163         195             200             205
165 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
166     210             215             220
168 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
169 225             230             235             240
171 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
172             245             250             255
174 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
175         260             265             270
177 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
178         275             280             285
180 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
181     290             295             300
183 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
184 305             310             315             320
186 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
187             325             330             335
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 657
191 <212> TYPE: DNA
192 <213> ORGANISM: H.Sapiens
194 <400> SEQUENCE: 3
195 cagcgcgagc gccttcatgg tgacggtgtc catgcgctgg cagtgtctgc gtgccacccg      60
197 gtgcacctgg agcgaggtga ggcagagcac cgccagcggc agcacgaagc ccacggcatg     120
199 gagcgtggcg gtgaaggctg cgaagcgcgg acgctcaggc tcgggcggca ggcgcagcga     180
201 acaggacgcg aaggcgctgc tgtagccaag ccacgagcag ccaagtgcag cgcctgagaa     240
203 ggccagcgac tgtccccagg cacagcccag cagcaggccg gcatagcgcg gtcgcaggcg     300
205 tccggcgtag cgcagtggga agcccactgc cagccactgg tctgcgctca gcgccgccac     360
207 gctcagcgcc gcgttggacg ccaggaaggt gtccaggaag ccaatgactt ggcatgcgcc     420
209 gggcgccgac ggtgtccgcc cgcgcatcac accgagcagc gtgaaggca tgtccagcgc     480
211 cgccagcagc aggtggccca gagacagatt caccagggag acgcctgagg ctcgagtgcg     540
213 gagctcagcg ctgtaggcgc aacaaagcag caccagtgcg ttggatagca gcgccacggc     600
215 cagtaccatc accaggagac ccgccagcag cgcctcgccg gggcccatgg cgctagc      657
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 217
220 <212> TYPE: PRT
221 <213> ORGANISM: H.Sapiens
223 <400> SEQUENCE: 4
225 Ser Ala Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met
226 1             5               10              15
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/714,449

DATE: 12/01/2000
TIME: 12:30:04

Input Set : A:\00431PHRM293.txt
Output Set: N:\CRF3\12012000\I714449.raw

```
228 Val Leu Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys
229          20                  25                      30
231 Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val
232          35                  40                      45
234 Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe
235          50                  55                      60
237 Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala
238 65                   70                  75                    80
240 Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala
241              85                  90                      95
243 Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe
244          100                 105                     110
246 Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu
247          115                 120                     125
249 Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu
250      130                 135                 140
252 Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu
253 145             150                 155                 160
255 Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala
256              165                 170                 175
258 Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu
259              180                 185                 190
261 Thr Ser Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met
262      195                 200                     205
264 Asp Thr Val Thr Met Lys Ala Leu Ala
265 -    210                 215
267 <210> SEQ ID NO: 5
268 <211> LENGTH: 222
269 <212> TYPE: DNA
270 <213> ORGANISM: H.Sapiens
272 <400> SEQUENCE: 5
273 tgtgcaggtg tgatctccat tcctttgtac atccctcaca cgctgttcga atgggatttt    60
275 ggaaaggaaa tctgtgtatt ttggctcact actgactatc tgttatgtac agcatctgta   120
277 tataacattg tcctcatcag ctatgatcga tacctgtcag tctcaaatgc tgtaagtcga   180
279 acacattaat ttatccccct tagaagatta tgtaaatgta ta                      222
282 <210> SEQ ID NO: 6
283 <211> LENGTH: 73
284 <212> TYPE: PRT
285 <213> ORGANISM: H.Sapiens
287 <400> SEQUENCE: 6
289 Cys Ala Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe
290 1            5                   10                  15
292 Glu Trp Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp
293          20                  25                      30
295 Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr
296          35                  40                      45
298 Asp Arg Tyr Leu Ser Val Ser Asn Ala Val Ser Arg Thr His Phe Ile
299      50                  55                      60
301 Pro Leu Arg Arg Leu Cys Lys Cys Ile
```

```
          RAW SEQUENCE LISTING              DATE: 12/01/2000
          PATENT APPLICATION:  US/09/714,449     TIME: 12:30:04

          Input Set : A:\00431PHRM293.txt
          Output Set: N:\CRF3\12012000\I714449.raw

302 65                      70
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 507
306 <212> TYPE: DNA
307 <213> ORGANISM: H.Sapiens
309 <400> SEQUENCE: 7
310 gacgtcgaag caggtgatga tgcccagggc gtgcaccggg taggtgagat cggtgcgcgc      60
312 cagcgggggac agggcggtca ggagcagcag ccaggtccct gcacacgcgg ccaccgcgta     120
314 acgacggcgg cgccagcgct tggagctgag cgggtacagg atccccagga agcgctccac      180
316 gctgatacag gtcatggtga ggatgctgga atacatgttt gcgtaaaagg ccacggtcac      240
318 cacgttgcaa agcagcaccc cgaataccca gtggtggcgg ttgcaatggt agtagatttg      300
320 gaaaggcaac acgctggcca gcatcaggtc cgtgacgctc aggttgatca tgaagatgac      360
322 cgacgggggat ctgggcccca tgccgcggca cagcacccac agagagaaga ggttgcccgg     420
324 gatgctgacc gccgccacca gcgagtacac cacgggcagg gccaccgcga tcgccgggtt      480
326 ccgcagcatc tgcagcgtcg cgttgtc                                          507
329 <210> SEQ ID NO: 8
330 <211> LENGTH: 169
331 <212> TYPE: PRT
332 <213> ORGANISM: H.Sapiens
334 <400> SEQUENCE: 8
336 Asp Asn Ala Thr Leu Gln Met Leu Arg Asn Pro Ala Ile Ala Val Ala
337 1               5                   10                  15
339 Leu Pro Val Val Tyr Ser Leu Val Ala Ala Val Ser Ile Pro Gly Asn
340             20                  25                  30
342 Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro
343         35                  40                  45
345 Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala
346     50                  55                  60
348 Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp
349 65                  70                  75                  80
351 Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala
352                 85                  90                  95
354 Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg
355             100                 105                 110
357 Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg
358         115                 120                 125
360 Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr
361     130                 135                 140
363 Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala
364 145                 150                 155                 160
366 Leu Gly Ile Ile Thr Cys Phe Asp Val
367                 165
369 <210> SEQ ID NO: 9
370 <211> LENGTH: 270
371 <212> TYPE: DNA
372 <213> ORGANISM: H.Sapiens
374 <400> SEQUENCE: 9
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377 gccgccaaca tcctactgtc ggggccgctc acgctgaaac tgtcccccgc gctctggttc     120
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```
<210>   117
<211>   20
<212>   DNA
<213>   Artificial Sequence
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see item 12 on Error Summary Sheet

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<400>   117
acagccccaa agccaaacac                                              20
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<211>   22
<212>   DNA
<213>   Artificial Sequence
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```
<400>   118
ccgcaggagc aatgaaaatc ag                                           22
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```
<210>   119
<211>   19
<212>   DNA
<213>   Artificial Sequence
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<400>   119
ctgaaagttg tcgctgacc                                               19
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These errors exist in subsequent sequences, too.

Please edit.

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L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:666 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:4417 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4417 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4426 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4426 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4435 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4435 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4458 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4458 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4608 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4608 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4631 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:4631 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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